

SEQUENCE LISTING

<110> Tait, Jonathan F.
Brown, David S.

<120> Annexin Derivatives with Endogenous Chelation Sites

<130> uofw-1-13841

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<170> PatentIn Ver. 2.0

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<211> 981

<212> DNA

<213> Homo sapiens

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<222> (1)..(981)

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Lys Ala Met Lys Gly Leu Gly Thr Asp Glu Glu Ser Ile Leu Thr Leu
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gct caa gtt gaa caa gat gct cag gct tta ttt cag gct gga gaa ctt 576
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 195 200 205

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280

285

ttt aac atc agg aag gag ttt agg aag aat ttt gcc acc tct ctt tat 912
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tcc atg att aag gga gat aca tct ggg gac tat aag aaa gct ctt ctg 960
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Leu Thr Ser Arg Ser Asn Ala Gln Arg Gln Glu Ile Ser Ala Ala Phe
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Leu Tyr Asp Ala Tyr Glu Leu Lys His Ala Leu Lys Gly Ala Gly Thr
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145 150 155 160

Val Val Leu Leu Gln Ala Asn Arg Asp Pro Asp Ala Gly Ile Asp Glu
165 170 175

Ala Gln Val Glu Gln Asp Ala Gln Ala Leu Phe Gln Ala Gly Glu Leu
180 185 190

Lys Trp Gly Thr Asp Glu Glu Lys Phe Ile Thr Ile Phe Gly Thr Arg
195 200 205

Ser Val Ser His Leu Arg Lys Val Phe Asp Lys Tyr Met Thr Ile Ser
210 215 220

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225 230 235 240

Glu Gln Leu Leu Leu Ala Val Val Lys Ser Ile Arg Ser Ile Pro Ala
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Tyr Leu Ala Glu Thr Leu Tyr Tyr Ala Met Lys Gly Ala Gly Thr Asp
260 265 270

Asp His Thr Leu Ile Arg Val Met Val Ser Arg Ser Glu Ile Asp Leu
275 280 285

Phe Asn Ile Arg Lys Glu Phe Arg Lys Asn Phe Ala Thr Ser Leu Tyr
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Leu Leu Ser Gly Glu Asp Asp
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 100 105 110

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Lys Ala Met Lys Gly Leu Gly Thr Asp Glu Glu Ser Ile Leu Thr Leu
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 Leu Thr Ser Arg Ser Asn Ala Gln Arg Gln Glu Ile Ser Ala Ala Phe
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 Lys Thr Leu Phe Gly Arg Asp Leu Leu Asp Asp Leu Lys Ser Glu Leu
 65 70 75 80
 Thr Gly Lys Phe Glu Lys Leu Ile Val Ala Leu Met Lys Pro Ser Arg
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 Leu Tyr Asp Ala Tyr Glu Leu Lys His Ala Leu Lys Gly Ala Gly Thr
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 Asn Glu Lys Val Leu Thr Glu Ile Ile Ala Ser Arg Thr Pro Glu Glu
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 Leu Arg Ala Ile Lys Gln Val Tyr Glu Glu Glu Tyr Gly Ser Ser Leu
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 Val Val Leu Leu Gln Ala Asn Arg Asp Pro Asp Ala Gly Ile Asp Glu
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 Ala Gln Val Glu Gln Asp Ala Gln Ala Leu Phe Gln Ala Gly Glu Leu
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 Lys Trp Gly Thr Asp Glu Glu Lys Phe Ile Thr Ile Phe Gly Thr Arg
 195 200 205
 Ser Val Ser His Leu Arg Lys Val Phe Asp Lys Tyr Met Thr Ile Ser
 210 215 220
 Gly Phe Gln Ile Glu Glu Thr Ile Asp Arg Glu Thr Ser Gly Asn Leu
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 Glu Gln Leu Leu Leu Ala Val Val Lys Ser Ile Arg Ser Ile Pro Ala
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 Tyr Leu Ala Glu Thr Leu Tyr Tyr Ala Met Lys Gly Ala Gly Thr Asp
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 Asp His Thr Leu Ile Arg Val Met Val Ser Arg Ser Glu Ile Asp Leu
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Phe Asn Ile Arg Lys Glu Phe Arg Lys Asn Phe Ala Thr Ser Leu Tyr
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Leu Leu Ser Gly Glu Asp Asp
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ttg aca tcc cga agt aat gct cag cgc cag gaa atc tct gca gct ttt 192
 Leu Thr Ser Arg Ser Asn Ala Gln Arg Gln Glu Ile Ser Ala Ala Phe
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 65 70 75 80

act gga aaa ttt gaa aaa tta att gtg gct ctg atg aaa ccc tct cgg 288
 Thr Gly Lys Phe Glu Lys Leu Ile Val Ala Leu Met Lys Pro Ser Arg
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ctt tat gat gct tat gaa ctg aaa cat gcc ttg aag gga gct gga aca 336
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aat gaa aaa gta ctg aca gaa att att gct tca agg aca cct gaa gaa	384
Asn Glu Lys Val Leu Thr Glu Ile Ile Ala Ser Arg Thr Pro Glu Glu	
115 120 125	
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Ala Gln Val Glu Gln Asp Ala Gln Ala Leu Phe Gln Ala Gly Glu Leu	
180 185 190	
aaa tgg ggg aca gat gaa gaa aag ttt atc acc atc ttt gga aca cga	624
Lys Trp Gly Thr Asp Glu Glu Lys Phe Ile Thr Ile Phe Gly Thr Arg	
195 200 205	
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225 230 235 240	
gag caa cta ctc ctt gct gtt gtg aaa tct att cga agt ata cct gcc	768
Glu Gln Leu Leu Leu Ala Val Val Lys Ser Ile Arg Ser Ile Pro Ala	
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tac ctt gca gag acc ctc tat tat gct atg aag gga gct ggg aca gat	816
Tyr Leu Ala Glu Thr Leu Tyr Tyr Ala Met Lys Gly Ala Gly Thr Asp	
260 265 270	
gat cat acc ctc atc aga gtc atg gtt tcc agg agt gag att gat ctg	864
Asp His Thr Leu Ile Arg Val Met Val Ser Arg Ser Glu Ile Asp Leu	
275 280 285	
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Phe Asn Ile Arg Lys Glu Phe Arg Lys Asn Phe Ala Thr Ser Leu Tyr	
290 295 300	

tcc atg att aag gga gat aca tct ggg gac tat aag aaa gct ctt ctg 960
 Ser Met Ile Lys Gly Asp Thr Ser Gly Asp Tyr Lys Lys Ala Leu Leu
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<210> 6

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 35 40 45

Leu Thr Ser Arg Ser Asn Ala Gln Arg Gln Glu Ile Ser Ala Ala Phe
 50 55 60

Lys Thr Leu Phe Gly Arg Asp Leu Leu Asp Asp Leu Lys Ser Glu Leu
 65 70 75 80

Thr Gly Lys Phe Glu Lys Leu Ile Val Ala Leu Met Lys Pro Ser Arg
 85 90 95

Leu Tyr Asp Ala Tyr Glu Leu Lys His Ala Leu Lys Gly Ala Gly Thr
 100 105 110

Asn Glu Lys Val Leu Thr Glu Ile Ile Ala Ser Arg Thr Pro Glu Glu
 115 120 125

Leu Arg Ala Ile Lys Gln Val Tyr Glu Glu Glu Tyr Gly Ser Ser Leu
 130 135 140

Glu Asp Asp Val Val Gly Asp Thr Ser Gly Tyr Tyr Gln Arg Met Leu
 145 150 155 160

Val Val Leu Leu Gln Ala Asn Arg Asp Pro Asp Ala Gly Ile Asp Glu
 165 170 175

Ala Gln Val Glu Gln Asp Ala Gln Ala Leu Phe Gln Ala Gly Glu Leu	180	185	190
Lys Trp Gly Thr Asp Glu Glu Lys Phe Ile Thr Ile Phe Gly Thr Arg	195	200	205
Ser Val Ser His Leu Arg Lys Val Phe Asp Lys Tyr Met Thr Ile Ser	210	215	220
Gly Phe Gln Ile Glu Glu Thr Ile Asp Arg Glu Thr Ser Gly Asn Leu	225	230	235 240
Glu Gln Leu Leu Leu Ala Val Val Lys Ser Ile Arg Ser Ile Pro Ala	245	250	255
Tyr Leu Ala Glu Thr Leu Tyr Tyr Ala Met Lys Gly Ala Gly Thr Asp	260	265	270
Asp His Thr Leu Ile Arg Val Met Val Ser Arg Ser Glu Ile Asp Leu	275	280	285
Phe Asn Ile Arg Lys Glu Phe Arg Lys Asn Phe Ala Thr Ser Leu Tyr	290	295	300
Ser Met Ile Lys Gly Asp Thr Ser Gly Asp Tyr Lys Lys Ala Leu Leu	305	310	315 320
Leu Leu Ser Gly Glu Asp Asp	325		

SEQUENCE LISTING

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Brown, David

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<140> US 09/324,096

<141> 1999-06-01

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<170> PatentIn version 3.0

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<221> CDS

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Met Ala Cys Gly Gly Gly His Met Ala Gln Val Leu Arg Gly Thr Val

1

5

10

15

act gac ttc cct gga ttt gat gag cgg gct gat gca gaa act ctt cgg

96

Thr Asp Phe Pro Gly Phe Asp Glu Arg Ala Asp Ala Glu Thr Leu Arg

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25

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aag gct atg aaa ggc ttg ggc aca gat gag gag agc atc ctg act ctg

144

Lys Ala Met Lys Gly Leu Gly Thr Asp Glu Glu Ser Ile Leu Thr Leu

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ttg aca tcc cga agt aat gct cag cgc cag gaa atc tct gca gct ttt

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aag act ctg ttt ggc agg gat ctt ctg gat gac ctg aaa tca gaa cta

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act gga aaa ttt gaa aaa tta att gtg gct ctg atg aaa ccc tct cgg

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90

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Leu Tyr Asp Ala Tyr Glu Leu Lys His Ala Leu Lys Gly Ala Gly Thr

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aat gaa aaa gta ctg aca gaa att att gct tca agg aca cct gaa gaa

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Asn Glu Lys Val Leu Thr Glu Ile Ile Ala Ser Arg Thr Pro Glu Glu

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185

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624

Lys Trp Gly Thr Asp Glu Glu Lys Phe Ile Thr Ile Phe Gly Thr Arg

195

200

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agt gtg tct cat ttg aga aag gtg ttt gac aag tac atg act ata tca

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215

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250

255

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816

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260

265

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Asp His Thr Leu Ile Arg Val Met Val Ser Arg Ser Glu Ile Asp Leu

275

280

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ttt aac atc agg aag gag ttt agg aag aat ttt gcc acc tct ctt tat

912

Phe Asn Ile Arg Lys Glu Phe Arg Lys Asn Phe Ala Thr Ser Leu Tyr

290

295

300

tcc atg att aag gga gat aca tct ggg gac tat aag aaa gct ctt ctg

960

Ser Met Ile Lys Gly Asp Thr Ser Gly Asp Tyr Lys Lys Ala Leu Leu

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ctg ctc tcc gga gaa gat gac

981

Leu Leu Ser Gly Glu Asp Asp

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<212> PRT

<213> Homo sapiens

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Lys Thr Leu Phe Gly Arg Asp Leu Leu Asp Asp Leu Lys Ser Glu Leu
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Thr Gly Lys Phe Glu Lys Leu Ile Val Ala Leu Met Lys Pro Ser Arg
85 90 95

Leu Tyr Asp Ala Tyr Glu Leu Lys His Ala Leu Lys Gly Ala Gly Thr
100 105 110

Asn Glu Lys Val Leu Thr Glu Ile Ile Ala Ser Arg Thr Pro Glu Glu
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Leu Arg Ala Ile Lys Gln Val Tyr Glu Glu Glu Tyr Gly Ser Ser Leu
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195 200 205

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245 250 255

Tyr Leu Ala Glu Thr Leu Tyr Tyr Ala Met Lys Gly Ala Gly Thr Asp
260 265 270

Asp His Thr Leu Ile Arg Val Met Val Ser Arg Ser Glu Ile Asp Leu
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Phe Asn Ile Arg Lys Glu Phe Arg Lys Asn Phe Ala Thr Ser Leu Tyr
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Leu Leu Ser Gly Glu Asp Asp
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96
 Thr Asp Phe Pro Gly Phe Asp Glu Arg Ala Asp Ala Glu Thr Leu Arg

20 25 30

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192

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240

Lys Thr Leu Phe Gly Arg Asp Leu Leu Asp Asp Leu Lys Ser Glu Leu

65

70

75

80

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288

Thr Gly Lys Phe Glu Lys Leu Ile Val Ala Leu Met Lys Pro Ser Arg

85

90

95

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336

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100

105

110

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384

Asn Glu Lys Val Leu Thr Glu Ile Ile Ala Ser Arg Thr Pro Glu Glu

115

120

125

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432

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528

Val Val Leu Leu Gln Ala Asn Arg Asp Pro Asp Ala Gly Ile Asp Glu

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170

175

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576

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180

185

190

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624

Lys Trp Gly Thr Asp Glu Glu Lys Phe Ile Thr Ile Phe Gly Thr Arg

195

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205

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672

Ser Val Ser His Leu Arg Lys Val Phe Asp Lys Tyr Met Thr Ile Ser

210

215

220

gga ttt caa att gag gaa acc att gac cgc gag act tct ggc aat tta

720

Gly Phe Gln Ile Glu Glu Thr Ile Asp Arg Glu Thr Ser Gly Asn Leu

225

230

235

240

gag caa cta ctc ctt gct gtt gtg aaa tct att cga agt ata cct gcc

768

Glu Gln Leu Leu Leu Ala Val Val Lys Ser Ile Arg Ser Ile Pro Ala

245

250

255

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816

Tyr Leu Ala Glu Thr Leu Tyr Tyr Ala Met Lys Gly Ala Gly Thr Asp

260

265

270

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864

Asp His Thr Leu Ile Arg Val Met Val Ser Arg Ser Glu Ile Asp Leu

275

280

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912

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295

300

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35 40 45Leu Thr Ser Arg Ser Asn Ala Gln Arg Gln Glu Ile Ser Ala Ala Phe
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Lys Thr Leu Phe Gly Arg Asp Leu Leu Asp Asp Leu Lys Ser Glu Leu
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Thr Gly Lys Phe Glu Lys Leu Ile Val Ala Leu Met Lys Pro Ser Arg
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Leu Tyr Asp Ala Tyr Glu Leu Lys His Ala Leu Lys Gly Ala Gly Thr
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Asn Glu Lys Val Leu Thr Glu Ile Ile Ala Ser Arg Thr Pro Glu Glu
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Glu Asp Asp Val Val Gly Asp Thr Ser Gly Tyr Tyr Gln Arg Met Leu
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180 185 190

Lys Trp Gly Thr Asp Glu Glu Lys Phe Ile Thr Ile Phe Gly Thr Arg
195 200 205

Ser Val Ser His Leu Arg Lys Val Phe Asp Lys Tyr Met Thr Ile Ser
210 215 220

Gly Phe Gln Ile Glu Glu Thr Ile Asp Arg Glu Thr Ser Gly Asn Leu
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Glu Gln Leu Leu Leu Ala Val Val Lys Ser Ile Arg Ser Ile Pro Ala
245 250 255

Tyr Leu Ala Glu Thr Leu Tyr Tyr Ala Met Lys Gly Ala Gly Thr Asp
260 265 270

Asp His Thr Leu Ile Arg Val Met Val Ser Arg Ser Glu Ile Asp Leu
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Phe Asn Ile Arg Lys Glu Phe Arg Lys Asn Phe Ala Thr Ser Leu Tyr
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 Lys Ala Met Lys Gly Leu Gly Thr Asp Glu Glu Ser Ile Leu Thr Leu

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Thr Gly Lys Phe Glu Lys Leu Ile Val Ala Leu Met Lys Pro Ser Arg

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336

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Leu Arg Ala Ile Lys Gln Val Tyr Glu Glu Glu Tyr Gly Ser Ser Leu

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Glu Asp Asp Val Val Gly Asp Thr Ser Gly Tyr Tyr Gln Arg Met Leu

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Val Val Leu Leu Gln Ala Asn Arg Asp Pro Asp Ala Gly Ile Asp Glu

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Ala Gln Val Glu Gln Asp Ala Gln Ala Leu Phe Gln Ala Gly Glu Leu

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Lys Trp Gly Thr Asp Glu Glu Lys Phe Ile Thr Ile Phe Gly Thr Arg

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agt gtg tct cat ttg aga aag gtg ttt gac aag tac atg act ata tca

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Ser Val Ser His Leu Arg Lys Val Phe Asp Lys Tyr Met Thr Ile Ser

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gga ttt caa att gag gaa acc att gac cgc gag act tct ggc aat tta

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Gly Phe Gln Ile Glu Glu Thr Ile Asp Arg Glu Thr Ser Gly Asn Leu

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Glu Gln Leu Leu Leu Ala Val Val Lys Ser Ile Arg Ser Ile Pro Ala

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Tyr Leu Ala Glu Thr Leu Tyr Tyr Ala Met Lys Gly Ala Gly Thr Asp

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gat cat acc ctc atc aga gtc atg gtt tcc agg agt gag att gat ctg

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Asp His Thr Leu Ile Arg Val Met Val Ser Arg Ser Glu Ile Asp Leu

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Phe Asn Ile Arg Lys Glu Phe Arg Lys Asn Phe Ala Thr Ser Leu Tyr

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Ser Met Ile Lys Gly Asp Thr Ser Gly Asp Tyr Lys Lys Ala Leu Leu

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<213> Homo sapiens

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20 25 30Lys Ala Met Lys Gly Leu Gly Thr Asp Glu Glu Ser Ile Leu Thr Leu
35 40 45Leu Thr Ser Arg Ser Asn Ala Gln Arg Gln Glu Ile Ser Ala Ala Phe
50 55 60

Lys Thr Leu Phe Gly Arg Asp Leu Leu Asp Asp Leu Lys Ser Glu Leu
65 70 75 80

Thr Gly Lys Phe Glu Lys Leu Ile Val Ala Leu Met Lys Pro Ser Arg
85 90 95

Leu Tyr Asp Ala Tyr Glu Leu Lys His Ala Leu Lys Gly Ala Gly Thr
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Asn Glu Lys Val Leu Thr Glu Ile Ile Ala Ser Arg Thr Pro Glu Glu
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Leu Arg Ala Ile Lys Gln Val Tyr Glu Glu Glu Tyr Gly Ser Ser Leu
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Glu Asp Asp Val Val Gly Asp Thr Ser Gly Tyr Tyr Gln Arg Met Leu
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Val Val Leu Leu Gln Ala Asn Arg Asp Pro Asp Ala Gly Ile Asp Glu
165 170 175

Ala Gln Val Glu Gln Asp Ala Gln Ala Leu Phe Gln Ala Gly Glu Leu
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Lys Trp Gly Thr Asp Glu Glu Lys Phe Ile Thr Ile Phe Gly Thr Arg
195 200 205

Ser Val Ser His Leu Arg Lys Val Phe Asp Lys Tyr Met Thr Ile Ser
210 215 220

Gly Phe Gln Ile Glu Glu Thr Ile Asp Arg Glu Thr Ser Gly Asn Leu
225 230 235 240

Glu Gln Leu Leu Leu Ala Val Val Lys Ser Ile Arg Ser Ile Pro Ala
245 250 255

Tyr Leu Ala Glu Thr Leu Tyr Tyr Ala Met Lys Gly Ala Gly Thr Asp
260 265 270

Asp His Thr Leu Ile Arg Val Met Val Ser Arg Ser Glu Ile Asp Leu
 275 280 285

Phe Asn Ile Arg Lys Glu Phe Arg Lys Asn Phe Ala Thr Ser Leu Tyr
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